IN THE CLAIMS:

Please amend the claims as indicated below.

1. (Previously Presented) A method for spatially profiling a protein to determine if the protein is a globular protein, the method comprising the steps of:

determining a spatial hydrophobicity distribution of the protein;

shifting the hydrophobicity distribution based on a difference between values in the hydrophobicity distribution and an average hydrophobicity value;

determining an adjusted second-order moment of hydrophobicity;

determining a profile of the second-order moment of hydrophobicity; and

comparing the profile to a globular protein profile to determine if the protein is a globular protein.

2. (Original) The method of claim 1, wherein the step of shifting the hydrophobicity distribution comprises the step of shifting the hydrophobicity distribution such that a total hydrophobicity of the protein is zero.

3. (Original) The method of claim 2, further comprising the step of normalizing the shifted hydrophobicity distribution, thereby causing a standard deviation of the shifted hydrophobicity distribution to be unity.

4. (Previously Presented) The method of claim 1, further comprising the steps of:

determining an adjusted zero-order moment of hydrophobicity;

determining a profile of the adjusted zero-order moment of hydrophobicity;

determining a first distance at which a maximum peak of the profile of the adjusted zero-order moment of hydrophobicity occurs and a first distance at which a maximum peak of the profile of the adjusted second-order moment of hydrophobicity occurs;

determining a second distance at which the adjusted zero-order moment of hydrophobicity vanishes and a second distance at which the adjusted second-order moment of hydrophobicity vanishes;

determining at least one ratio between at least one of the first second-order moment distance and the first zero-order moment distance, and the second second-order moment distance and the second zero-order moment distance; and

comparing the at least one ratio to one or more globular protein ratios to determine if the protein is a globular protein.

5. (Cancelled)

6. (Previously Presented) The method of claim 1, wherein the step of determining a spatial hydrophobicity distribution of a protein comprises the step of assigning a hydrophobicity value to each of a plurality of residues of the protein.

7. (Cancelled)

8. (Cancelled)

9. (Cancelled)

10. (Cancelled)

11. (Cancelled)

12. (Cancelled)

13. (Cancelled)

14. (Cancelled)

15. (Cancelled)

16. (Cancelled)

17. (Cancelled)

18. (Cancelled)

19. (Cancelled)

20. (Cancelled)

21. (Cancelled)

22. (Previously Presented) A system comprising:

a memory that stores computer-readable code; and

a processor operatively coupled to the memory, the processor configured to implement the computer-readable code, the computer-readable code configured to:

determine a spatial hydrophobicity distribution of a protein;

shift the hydrophobicity distribution based on a difference between values in the hydrophobicity distribution and an average hydrophobicity value;

determine an adjusted second-order moment of hydrophobicity;

determine a profile of the second-order moment of hydrophobicity; and

compare the profile to a globular protein profile to determine if the protein is a globular protein.

23. (Original) The system of claim 22, wherein the computer-readable code is further configured, when shifting the hydrophobicity distribution, to shift the hydrophobicity distribution such that a total hydrophobicity of the protein is zero.

24. (Original) The system of claim 23, wherein the computer-readable code is further configured to normalize the shifted hydrophobicity distribution, thereby causing a standard deviation of the shifted hydrophobicity distribution to be unity.

25. (Previously Presented) The system of claim 22, wherein the computer-readable code is further configured to:

determine an adjusted zero-order moment of hydrophobicity;

determine a profile of the adjusted zero-order moment of hydrophobicity;

determine a first distance at which a maximum peak of the profile of the adjusted zero-order moment of hydrophobicity occurs and a first distance at which a maximum peak of the profile of the adjusted second-order moment of hydrophobicity occurs;

determine a second distance at which the adjusted zero-order moment of hydrophobicity vanishes and a second distance at which the adjusted second-order moment of hydrophobicity vanishes;

determine at least one ratio between at least one of the first second-order moment distance and the first zero-order moment distance, and the second second-order moment distance and the second zero-order moment distance; and

compare the at least one ratio to one or more globular protein ratios to determine if the protein is a globular protein.

26. (Cancelled)

27. (Previously Presented) The system of claim 22, wherein the computer-readable code is further configured, when determining a spatial hydrophobicity distribution of a protein, to assign a hydrophobicity value to each of a plurality of residues of the protein.

28. (Cancelled)

29. (Cancelled)

30. (Cancelled)

31. (Cancelled)

32. (Cancelled)

33. (Previously Presented) An article of manufacture comprising:

a computer-readable medium having computer-readable code embodied thereon, the computer-readable code comprising:

a step to determine a spatial hydrophobicity distribution of a protein;

a step to shift the hydrophobicity distribution based on a difference between values in the hydrophobicity distribution and an average hydrophobicity value;

a step to determine an adjusted second-order moment of hydrophobicity;

a step to determine a profile of the second-order moment of hydrophobicity; and

a step to compare the profile to a globular protein profile to determine if the protein is a globular protein.

34. (Original) The article of manufacture of claim 33, wherein the computer-readable code further comprises, when shifting the hydrophobicity distribution, a step to shift the hydrophobicity distribution such that a total hydrophobicity of the protein is zero.

35. (Original) The article of manufacture of claim 34, wherein the computer-readable code further comprises a step to normalize the shifted hydrophobicity distribution, thereby causing a standard deviation of the shifted hydrophobicity distribution to be unity.

36. (Previously Presented) The article of manufacture of claim 33, wherein the computer-readable further comprises:

a step to determine an adjusted zero-order moment of hydrophobicity;

a step to determine a profile of the adjusted zero-order moment of hydrophobicity;

a step to determine a first distance at which a maximum peak of the profile of the adjusted zero-order moment of hydrophobicity occurs and a first distance at which a maximum peak of the profile of the adjusted second-order moment of hydrophobicity occurs;

a step to determine a second distance at which the adjusted zero-order moment of hydrophobicity vanishes and a second distance at which the adjusted second-order moment of hydrophobicity vanishes;

a step to determine at least one ratio between at least one of the first second-order moment distance and the first zero-order moment distance, and the second second-order moment distance and the second zero-order moment distance; and

a step to compare the at least one ratio to one or more globular protein ratios to determine if the protein is a globular protein.

37. (Cancelled)

38. (Previously Presented) The article of manufacture of claim 33, wherein the computer-readable code further comprises, when determining a spatial hydrophobicity distribution of a protein, a step to assign a hydrophobicity value to each of a plurality of residues of the protein.

39. (Cancelled)

40. (Cancelled)

41. (Cancelled)

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42. (Cancelled)

43. (Cancelled)